GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 03:48:38 ; Search time 10747 Seconds
(without alignments)
11760.816 Million cell updates/sec

Title: US-09-730-559B-7
Perfect score: 4343
Sequence: 1 atggacgccccaaaagcagg.....attcacagcagtcccctttct 4343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	3301.2	76.0	169377	9	AC027228	AC027228 Homo sapi
	2	1420.4	32.7	1546	9	BC017880	BC017880 Homo sapi
	3	1023	23.6	2889	9	HUMIREBPA	M58511 Human iron-
	4	1023	23.6	3280	6	AX400060	AX400060 Sequence
	5	990	22.8	2867	6	AX377520	AX377520 Sequence
	6	990	22.8	2867	9	HSU20180	U20180 Human iron-
	7	944.2	21.7	3341	9	AK027033	AK027033 Homo sapi
	8	877.2	20.2	3770	6	AX377522	AX377522 Sequence
	9	877.2	20.2	3770	10	RNU20181	U20181 Rattus norv
c	10	396.2	9.1	309562	2	AC004469	AC004469 Homo sapi
	11	385.4	8.9	176314	2	AC044886	AC044886 Homo sapi
	12	381.2	8.8	141037	9	AC096711	AC096711 Homo sapi
	13	380.2	8.8	183658	2	AC032021	AC032021 Homo sapi
c	14	380.2	8.8	186131	9	AL158192	AL158192 Human DNA
	15	377.6	8.7	170881	2	AC122718	AC122718 Homo sapi
c	16	377.2	8.7	92702	9	AC091829	AC091829 Homo sapi
	17	374.6	8.6	206454	9	AC018737	AC018737 Homo sapi
c	18	373.6	8.6	110000	2	AL390202_05	Continuation (6 of
	19	373.6	8.6	162609	9	AC108022	AC108022 Homo sapi
c	20	372.2	8.6	40182	9	AC092824	AC092824 Homo sapi
	21	372.2	8.6	159385	9	AC007619	AC007619 Homo sapi
c	22	371	8.5	155862	9	AC018464	AC018464 Homo sapi
	23	370.8	8.5	186321	9	AC006511	AC006511 Homo sapi
c	24	369	8.5	170330	9	AC092896	AC092896 Homo sapi
c	25	367.6	8.5	102837	9	HS522O2	Z95329 Human DNA s
	26	367.2	8.5	177647	9	AC091969	AC091969 Homo sapi
	27	366.8	8.4	99781	9	AF031078	AF031078 Homo sapi
	28	366.8	8.4	112756	9	AF030876	AF030876 Homo sapi
	29	364.4	8.4	195342	9	AC009120	AC009120 Homo sapi
c	30	364	8.4	166032	2	AC023645	AC023645 Homo sapi
c	31	363.6	8.4	86441	2	AL390762	AL390762 Homo sapi
c	32	363.6	8.4	100000	9	AP000519	AP000519 Homo sapi
c	33	363.6	8.4	162227	9	AB023056	AB023056 Homo sapi
	34	363.4	8.4	156399	9	AC002456	AC002456 Homo sapi
	35	361.8	8.3	175789	2	AP000425	AP000425 Homo sapi
	36	361.6	8.3	21896	9	AL591364	AL591364 Human DNA
c	37	360.6	8.3	153221	2	AC067998	AC067998 Homo sapi
c	38	360	8.3	134026	2	AC069317	AC069317 Homo sapi
	39	359.4	8.3	131928	9	AC091738	AC091738 Homo sapi
c	40	358.4	8.3	219357	9	AC107464	AC107464 Homo sapi
c	41	358.2	8.2	160302	2	AC129730	AC129730 Homo sapi
c	42	358.2	8.2	193970	2	AL357119	AL357119 Homo sapi
	43	356.6	8.2	116400	9	AC055752	AC055752 Homo sapi
	44	356.6	8.2	152528	2	AC016063	AC016063 Homo sapi
	45	355.6	8.2	162282	9	AC094095	AC094095 Homo sapi

ALIGNMENTS

RESULT 1
AC027228/c
LOCUS AC027228 169377 bp DNA linear PRI 06-AUG-2002
DEFINITION Homo sapiens chromosome 15, clone RP11-650L12, complete sequence.
ACCESSION AC027228
VERSION AC027228.16 GI:22024598
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 169377)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 15, clone RP11-650L12
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169377)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A.,.Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 3 (bases 1 to 169377)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 4 (bases 1 to 169377)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 5 (bases 1 to 169377)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jul 31, 2002 this sequence version replaced gi:21392498.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
---------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
---------- Project Information
Center project name: L8639
Center clone name: 650_L_12
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FEATURES	Location/Qualifiers
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	/chromosome="15"
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repeat_region	2162. .2206
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	/rpt_family="AluSq"
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	/rpt_family="AluSp"
repeat_region	complement(4684. .4972)
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	/rpt_family="L1PB1"
repeat_region	complement(5623. .5926)
	/rpt_family="AluSx"
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repeat_region	9364. .9808
	/rpt_family="L2"
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unsure	9784. .9794
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  Query Match             76.0%;  Score 3301.2;  DB 9;  Length 169377;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 3431;  Conservative    3;  Mismatches   31;  Indels   13;  Gaps   10;

Qy     872 TTCTGGGGTGGGGGGTTGGAGGCATTGAAACAGAAGCAGTTATGCTTGGTCTGCCAGTTT 931
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Qy     992 CATCCATAGATGTTGTTCTTGGTATTACAAAGGTAAGTTAAAGTTGTGGTAGCTCTATGA 1051
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Db  123664 CATCCATAGATGTTGTTCTTGGTATTACAAAGGTAAGTTAAAGTTGTGGTAGCTCTATGA 123605

Qy    1052 CTTACTGAACATTATTTTTATAAAAATTGAAGAGCTCTATGAGAGCAGGGATTTGGGTTC 1111
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Qy    1112 ATTACTGCATCCTCAGGTCTCTTGACGTTAGCCACATCATCATAGTTATCATAGTAATAA 1171
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Qy    1172 CAACAAACAGAGCATTTAGTTTGTACTAATAAATACAAAGAAATTTGTTGTGTTCACTTA 1231
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Qy    1232 TGTTAGCTCATTTAGTCCTTATAACAAGCCTGTGAGATGGATACTATTACTATTCTCATT 1291
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Db  123424 TGTTAGCTCATTTAGTCCTTATAACAAGCCTGTGAGATGGATACTATTACTATTCTCATT 123365

Qy    1292 GTAACTCTGAGAAAACTAAGGTACAGTAGGGTTTAGTGACTTACCAAAGGGTCGAAGGCC 1351
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Db  123364 GTAACTCTGAGAAAACTAAGGTACAGTAGGGTTTAGTGACTTACCAAAGGGTCGAAGGCC 123305

Qy    1352 TGAGTA-TAAGGGGTAGAGCAAAGATTCCAGGCAGTCAGATTCTTGAGTCATGT---CTA 1407
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Db  123304 TGAGTAGTAAGGGGTAGAGCAAAGATTCCAGGCAGTCAGATTCTTGAGTCCATTGTCTTA 123245

Qy    1408 ACCATTATGCCTTATTAGTGCCTTGTTGCCTTAATAAACACTTGCTGGACTACATATTTT 1467
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Qy    1468 TTTTCTCTTTTTTAACTTGAATTAAAAAAAAATGTTTAGCAAAAGTTGAWTGTGTCGTCT 1527
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Qy    1528 TTAATTAAATTATTTGCCCGTTAGAAACTGTTGCTCTACTAAGTAATGCTTTCAAAAACA 1587
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Qy    1588 TGGACTGTAGAAATGTGATATATCATTTTTCTGTTGCCGTTTTAACATTTCTCTGGATTA 1647
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Qy    1648 TTATGTAAAAATCTTCTCTCTGAATTTTTAAAATACTGGCTTCAGAACTTCAATACATAC 1707
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Qy    1768 GTAACTCTTCTTCCTAAATGTCTGGCCTTTGCTAACTTTATTTTAATGATTAAATCCTAT 1827
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Qy    1828 TTTGTTAAATGAATGTACCTGGAAAATGTTCCACATATAATTCCAATTTGAGTCCCAATC 1887
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Qy    1888 TCAGCATTTTTGGTTAGATTATTGGTACGAAGGCTTTCTGGATACTCCAGTGTAAGGAAA 1947
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Qy    1948 TGATAATGCCTCCCTCTCAGCATTTGGTATTGATCCTTCTTCCCTAATTAGAAAAGAATT 2007
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Qy    2008 TGGCATCTTAGAGAAATTATTGATTCAACGTATGATACCAAAAGATCAAGTAGTAAATTG 2067
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Db  122645 TGGCATCTTAGAGAAATTATTGATTCAACGTATGATACCAAAAGATCAAGTAGTAAATTG 122586

Qy    2068 GGAATTGCAGGATTATTCCTAGAGGAAAAGGAGTATCCCATTATGTTTTTACAGAAATCA 2127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  122585 GGAATTGCAGGATTATTCCTAGAGGAAAAGGAGTATCCCATTATGTTTTTACAGAAATCA 122526

Qy    2128 ATTCTTTACTTTAGACATCCTGAAAACTAACGCTGCTTTTTAGCCTTCTCTAGCTGTTTT 2187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  122525 ATTCTTTACTTTAGACATCCTGAAAACTAACGCTGCTTTTTAGCCTTCTCTAGCTGTTTT 122466

Qy    2188 TTCCTGACAATATTACTGTGTGTTTTTTGACATTTTAGTTTAATGTTAAAAAATTAATCT 2247
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Qy    2248 ATTATATATGTTTACATTTATTGAATATATTGATTACTTCTTTTTTGAGATCCTGTTCCA 2307
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Qy    2308 TTTGTGATCCTTATAGGAATAATCCTGTATTGTTTTTTTGATGAGAGCAGCATTTGGTTT 2367
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Db  122346 TTTGTGATCCTTATAGGAATAATCCTGTATTGTTTTTTTGATGAGAGCAGCATTTGGTTT 122287
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Qy   2368 GTAATATCTAATCTGTGTTTCTTTCATCCTAAAAAATAAAACCATAGGCCGGGCGCGGTG 2427
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Qy   2488 GATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATT 2547
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Qy   2548 AGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTTCTCGGGAGGCTGAGGCAGGAGAA 2607
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Qy   2608 TGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCAAGATTGCGCCACTGCAGTCCGCA 2667
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Db 122046 TGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCCACTGCAGTCCGCA 121987

Qy   2668 GTCCGGCCTGGGCGACAGAGCGAGACTCTGTYTCAAAAAAAAAAAAAAAAAAAAAAAAAC 2727
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Qy   2728 CATAAATGAGGAAACGCATCTTTACACTTAGGGTTTGAGTTTCTGTATCTATAAAAAAGG 2787
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Qy   2788 GTTTGGATTAAGTGATCCCTGGCACTTATAAAATGTTAGGGCTTAATATTATTCATAGAT 2847
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Db 121868 GTTTGGATTAAGTGATCCCTGGCACTTATAAAATGTTAGGGCTTAATATTATTCATAGAT 121809

Qy   2848 CGAGGATAGTTTCATTCTTAGTCGCCTCCTTAGTCACTCTTCCTATACCAATCTGAGACC 2907
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Qy   2908 ATTTTACAATTTAGAAAAGACAAATAACTGGTTGGGTTACTTGATAGTATAATAACCAAG 2967
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Db 121748 ATTTTACAATTTAGAAAAGACAAATAACTGGTTGGGTTACTTGATAGTATAATAACCAAG 121689

Qy   2968 AAAAATAATTTTAGAAGGAATTAAGTTTGAAACCACATGTTAACAAATTCTACCAAAGTG 3027
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Db 121688 AAAAATAATTTTAGAAGGAATTAAGTTTGAAACCACATGTTAACAAATTCTACCAAAGTG 121629

Qy   3028 GGATTTGCCTGTGATTAAAGATGCTGTAAACATTTGGGCCAGTAGTTATAATTTGAAAAA 3087
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Qy   3088 TGTTTATAGCCAATATATAATTTTTTATTTAAATATACAGTTTCATCAGTCTATTAGTAT 3147
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Qy   3448 CACACCACTGCGCTCCAGCGTGGGCAACAGAGTGAGACCCTGTTTCTAAAAGAAAGAAAG 3507
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Qy   3508 AAAAAAGGGCTGCCACCTAAACAGACACACTATTGAGTTGAGGTACCCTGATTTCAAAGA 3567
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Qy   3568 CATGAAAATGTTAATTATAGCCACCTTGAAGCTTTCAGGSCCCTTTCTACCCTGAATTAA 3627
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Qy   3628 CAGTGACATTGGACCAGTCTTCTCTTTACTTCTTATCTTAAAATACCCCCAAAACCAGAA 3687
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Qy   3688 TGAGTTGATTCATAAGGACAATGAAGGATCTCATTCCTTCACCATCACTAGTATTGGTTA 3747
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Qy   3748 AAAATTTTATTTTATAGTTTTCAGACAATCGTTGCTAATCTTATCTTTGCAATTTTGTAT 3807
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Db 120911 AAAATTTTATTTTATAGTTTTCAGACAATCGTTGCTAATCTTATCTTTGCAATTTTGTAT 120852

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Qy   3868 TGAGTTTTTTGGAAGTGGAGTTTCACAATTATCTATAGTTGATCGAACTACAATAGCAAA 3927
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Qy   3988 ACATTTAGAACATACAGGTAAGAAGATAAAAGATCACTAGAATAAACATGTTACATTTCC 4047
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Qy   4168 TGTCCTCAAACCCTAGTTCCCTGTGACACATTGAAAGCAATTTAAAGGAATTATTCAAAC 4227
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Db 120491 TGTCCTCAAACCCTAGTTCCCTGTGACACATTGAAAGCAATTTAAAGGAATTATTCAAAC 120432

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Qy   4287 TCATAGG-TGCAATTTAATGGAGTCAGCCCTTAAACATATTCACAGCAGTCCCCTTCT 4343
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RESULT 2
BC017880
LOCUS       BC017880               1546 bp    mRNA    linear   PRI 06-DEC-2001
DEFINITION  Homo sapiens, clone MGC:22754 IMAGE:4277855, mRNA, complete cds.
ACCESSION   BC017880
VERSION     BC017880.1  GI:17389723
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1546)
  AUTHORS   Strausberg,R.
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  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 35 Row: k Column: 1
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
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                     VVLGITKVS"
BASE COUNT      462 a    296 c    340 g    448 t
ORIGIN

  Query Match           32.7%;  Score 1420.4;  DB 9;  Length 1546;
  Best Local Similarity  99.3%;  Pred. No. 1.7e-288;
  Matches 1448;  Conservative    0;  Mismatches    6;  Indels    4;  Gaps    2;

Qy       1 ATGGACGCCCCAAAAGCAGGATACGCCTTTGAGTACCTTATTGAAACATTAAATGACAGT 60
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Qy    1321 GGTTTAGTGACTTACCAAAGGGTCGAAGGCCTGAGTA-TAAGGGGTAGAGCAAAGATTCC 1379
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Db    1435 AGGCAGTCAGATTCTTGAGTCCATTGTCTTAACCATTATGCCTTATTAGTGCCTTGTTGC 1494

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Db    1495 CTTAATAAACACTTGCTG 1512
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RESULT 3
HUMIREBPA
LOCUS       HUMIREBPA               2889 bp    mRNA    linear   PRI 14-JUL-1995
DEFINITION  Human iron-responsive element-binding protein/iron regulatory
            protein 2 (IRE-BP2/IRP2) mRNA, partial cds.
ACCESSION   M58511 M37836
VERSION     M58511.1  GI:897825
KEYWORDS    RNA regulatory protein; iron-responsive element-binding protein.
SOURCE      Human cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2889)
  AUTHORS   Rouault,T.A., Tang,C.K., Kaptain,S., Burgess,W.H., Haile,D.J.,
            Samaniego,F., McBride,O.W., Harford,J.B. and Klausner,R.D.
  TITLE     Cloning of the cDNA encoding an RNA regulatory protein--the human
            iron-responsive element-binding protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87 (20), 7958-7962 (1990)
  MEDLINE   91045916
   PUBMED   2172968
REFERENCE   2  (bases 1 to 2889)
  AUTHORS   Samaniego,F., Chin,J., Iwai,K., Rouault,T.A. and Klausner,R.D.
  TITLE     Molecular characterization of a second iron-responsive element
            binding protein, iron regulatory protein 2. Structure, function,
            and post-translational regulation
  JOURNAL   J. Biol. Chem. 269 (49), 30904-30910 (1994)
  MEDLINE   95074121
   PUBMED   7983023
REFERENCE   3  (bases 1 to 2889)
  AUTHORS   Rouault,T.A., Haile,D.J., Downey,W.E., Philpott,C.C., Tang,C.,
            Samaniego,F., Chin,J., Paul,I., Orloff,D., Harford,J.B. et al.
  TITLE     An iron-sulfur cluster plays a novel regulatory role in the
            iron-responsive element binding protein
  JOURNAL   Biometals 5 (3), 131-140 (1992)
  MEDLINE   93044098
   PUBMED   1421965
REFERENCE   4  (bases 1 to 2889)
  AUTHORS   Rouault,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1990) Tracey A. Rouault, Cell Biology and
            Metabolism Branch, NICHHD, NIH, Bethesda, MD 20992, USA
COMMENT     On Jul 14, 1995 this sequence version replaced gi:186547.
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BASE COUNT      879 a    534 c    637 g    839 t
ORIGIN
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  Query Match           23.6%;  Score 1023;  DB 9;  Length 2889;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-205;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGACGCCCCAAAAGCAGGATACGCCTTTGAGTACCTTATTGAAACATTAAATGACAGT 60
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Db      1 ATGGACGCCCCAAAAGCAGGATACGCCTTTGAGTACCTTATTGAAACATTAAATGACAGT 60

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Db    301 GCTATGAGGGAGGCAGTGAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTTGT 360

Qy    361 CCGACAGATCTTACAGTTGACCATTCTTTACAAATTGACTTCAGTAAATGTGCAATACAG 420
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Db    421 AATGCACCAAATCCTGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAA 480

Qy    481 GTGCAGCCTAAGAAGCTTCCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTCT 540
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Qy    541 GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGCAGATTGAGAATACACCCATCCTG 600
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Db    661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTAAGTGGAGTTCAAGAGTTTTAAAG 720

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Db    781 TCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTCTTCCCAGACAGTGTAGTCGGCACAGAT 840
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Qy    841 TCACACATAACGATGGTGAATGGTTTAGGGATTCTGGGGTGGGGGGTTGGAGGCATTGAA 900
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Qy    961 GAGTTAACTGGGTCATCAAACCCTTTTGTTACATCCATAGATGTTGTTCTTGGTATTACA 1020
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Qy   1021 AAG 1023
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Db   1021 AAG 1023
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RESULT 4
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LOCUS       AX400060                3280 bp    DNA     linear   PAT 06-JUN-2002
DEFINITION  Sequence 231 from Patent WO0218424.
ACCESSION   AX400060
VERSION     AX400060.1  GI:21336471
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,Y.T., Asundi,V., Zhou,P., Xue,A.J., Ren,F., Zhang,J.,
            Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T.
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO 0218424-A 231 07-MAR-2002;
            HYSEQ, INC. (US)
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                     VISCTNNCNPSVMLAAGLLAKKAVEAGLRVKPYIRTSLSPGSGMVTHYLSSSGVLPYL
                     SKLGFEIVGYGCSTCVGNTAPLSDAVLNAVKQGDLVTCGNFIWKKNFEGRLCDCVRAN
                     YLASPPLVVAYAIAGTVNIDFQTEPLGTDPTGKNIYLHDIWPSREEVHRVEEEHVILS
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                     HVLLYLGDSVTTDHISPAGSIARNSAAAKYLTNRGLTPREFNSYGARRGNDAVMTRGT
                     FANIKLFNKFIGKPAPKTIHFPSGQTLDVFEAAELYQKEGIPLIILAGKKYGSGNSRD
                     WAAKGPYLLGVKAVLAESYEKIHKDHLIGIGIAPLQFLPGENADSLGLSGRETFSLTF
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BASE COUNT     1009 a    594 c    713 g    964 t
ORIGIN
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  Query Match             23.6%;  Score 1023;  DB 6;  Length 3280;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-205;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGACGCCCCAAAAGCAGGATACGCCTTTGAGTACCTTATTGAAACATTAAATGACAGT 60
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Db      1 ATGGACGCCCCAAAAGCAGGATACGCCTTTGAGTACCTTATTGAAACATTAAATGACAGT 60

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Qy    181 GAAGATGTTATGAACATTTTAGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCCTTT 240
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Db    181 GAAGATGTTATGAACATTTTAGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCCTTT 240

Qy    241 TTCCCTGCCCGTGTTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGCT 300
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Qy    301 GCTATGAGGGAGGCAGTGAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTTGT 360
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Db    301 GCTATGAGGGAGGCAGTGAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTTGT 360

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Db    361 CCGACAGATCTTACAGTTGACCATTCTTTACAAATTGACTTCAGTAAATGTGCAATACAG 420

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Qy    541 GGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGCAGATTGAGAATACACCCATCCTG 600
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Qy    601 TGTCCTTTTCATTTGCAACCAGTGCCTGAACCTGAAACAGTGTTAAAAAATCAAGAAGTA 660
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Db    601 TGTCCTTTTCATTTGCAACCAGTGCCTGAACCTGAAACAGTGTTAAAAAATCAAGAAGTA 660

Qy    661 GAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTAAGTGGAGTTCAAGAGTTTTAAAG 720
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Qy    781 TCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTCTTCCCAGACAGTGTAGTCGGCACAGAT 840
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Db    901 ACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTCTTACTTTACCAGAGGTGGTTGGATGT 960

Qy    961 GAGTTAACTGGGTCATCAAACCCTTTTGTTACATCCATAGATGTTGTTCTTGGTATTACA 1020
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Db    961 GAGTTAACTGGGTCATCAAACCCTTTTGTTACATCCATAGATGTTGTTCTTGGTATTACA 1020

Qy   1021 AAG 1023
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Db   1021 AAG 1023
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RESULT 5
AX377520
LOCUS       AX377520                2867 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 17 from Patent WO0212284.
ACCESSION   AX377520
VERSION     AX377520.1  GI:19573708
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KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kirsch,W.M., Lennart,A., Kelln,W.J., Kang,D.K., Levine,R.L. and
            Roualt,T.A.
  TITLE     Iron regulating protein-2 (irp-2) as a diagnostic for
            neurodegenerative disease
  JOURNAL   Patent: WO 0212284-A 17 14-FEB-2002;
            Loma Linda University Medical Center (US) ; THE SECRETARY OF THE
            DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .2867
                     /organism="Homo sapiens"
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BASE COUNT      871 a    527 c    630 g    839 t
ORIGIN

  Query Match             22.8%;  Score 990;  DB 6;  Length 2867;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-198;
  Matches  990;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     601 GAAACAGTGTTAAAAAATCAAGAAGTAGAATTCGGCAGAAATCGAGAGAGGCTTCAGTTT 660

Qy     694 TTTAAGTGGAGTTCAAGAGTTTTAAAGAATGTGGCAGTGATCCCTCCTGGAACTGGAATG 753
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Db     961 TCCATAGATGTTGTTCTTGGTATTACAAAG 990


RESULT 6
HSU20180
LOCUS       HSU20180                2867 bp    mRNA    linear   PRI 26-OCT-1995
DEFINITION  Human iron-regulatory protein 2 (IRP2) mRNA, partial cds.
ACCESSION   U20180
VERSION     U20180.1  GI:897580
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2867)
  AUTHORS   Guo,B., Brown,F.M., Phillips,J.D., Yu,Y. and Leibold,E.A.
  TITLE     Characterization and expression of iron regulatory protein 2
            (IRP2). Presence of multiple IRP2 transcripts regulated by
            intracellular iron levels
  JOURNAL   J. Biol. Chem. 270 (28), 16529-16535 (1995)
  MEDLINE   95348066
   PUBMED   7622457
REFERENCE   2  (bases 1 to 2867)
  AUTHORS   Brown,F.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1995) Fritz M. Brown, Program in Hum. Mol. Biol.
            and Genetics, University of Utah, 3250 Bldg 533, Salt Lake City, UT
            84112, USA
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                     /sex="female"
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                     /dev_stage="fetus"
                     /note="Similar to GenBank Accession No. U20181"
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     CDS             <1. .2859
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                     KLESMETYLKAVKLFRNDQNSSGEPEYSQVIQINLNSIVPSVSGPKRPRDRVAVTDMK
                     SDFQACLNEKVGFKGFQIAAEKQKDIVSIHYEGSEYKLSHGSVVIAAVISCTNNCNPS
                     VMLAAGLLAKKAVEAGLRVKPYIRTSLSPGSGMVTHYLSSSGVLPYLSKLGFEIVGYG
                     CSTCVGNTAPLSDAVLNAVKQGDLVTCGNFIWKKNFEGRLCDCVRANYLASPPLVVAY
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                     AIAGTVNIDFQTEPLGTDPTGKNIYLHDIWPSREEVHRVEEEHVILSMFKALKDKIEM
                     GNKRWNSLEAPDSVLFPWDLKSTYIRCPSFFDKLTKEPIALQAIENAHVLLYLGDSVT
                     TDHISPAGSIARNSAAAKYLTNRGLTPREFNSYGARRGNDAVMTRGTFANIKLFNKFI
                     GKPAPKTIHFPSGQTLDVFEAAELYQKEGIPLIILAGKKYGSGNSRDWAAKGPYLLGV
                     KAVLAESYEKIHKDHLIGIGIAPLQFLPGENADSLGLSGRETFSLTFPEELSPGITLN
                     IQTSTGKVFSVIASFEDDVEITLYKHGGLLNFVARKFS"
BASE COUNT      871 a    527 c    630 g    839 t
ORIGIN

  Query Match             22.8%;  Score 990;  DB 9;  Length 2867;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-198;
  Matches  990;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      34 TACCTTATTGAAACATTAAATGACAGTTCACATAAGAAGTTCTTCGATGTATCTAAACTT 93
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTTATTGAAACATTAAATGACAGTTCACATAAGAAGTTCTTCGATGTATCTAAACTT 60

Qy      94 GGCACCAAGTATGATGTTCTGCCTTACTCAATACGGGTCTTGTTGGAAGCTGCTGTACGA 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCACCAAGTATGATGTTCTGCCTTACTCAATACGGGTCTTGTTGGAAGCTGCTGTACGA 120

Qy     154 AATTGTGATGGCTTTTTAATGAAGAAGGAAGATGTTATGAACATTTTAGACTGGAAAACC 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AATTGTGATGGCTTTTTAATGAAGAAGGAAGATGTTATGAACATTTTAGACTGGAAAACC 180

Qy     214 AAACAAAGCAATGTTGAAGTGCCCTTTTTCCCTGCCCGTGTTCTTCTTCAAGATTTTACT 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AAACAAAGCAATGTTGAAGTGCCCTTTTTCCCTGCCCGTGTTCTTCTTCAAGATTTTACT 240

Qy     274 GGAATACCAGCAATGGTGGATTTTGCTGCTATGAGGGAGGCAGTGAAAACTCTTGGAGGT 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGAATACCAGCAATGGTGGATTTTGCTGCTATGAGGGAGGCAGTGAAAACTCTTGGAGGT 300

Qy     334 GATCCTGAGAAAGTCCATCCTGCTTGTCCGACAGATCTTACAGTTGACCATTCTTTACAA 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GATCCTGAGAAAGTCCATCCTGCTTGTCCGACAGATCTTACAGTTGACCATTCTTTACAA 360

Qy     394 ATTGACTTCAGTAAATGTGCAATACAGAATGCACCAAATCCTGGAGGTGGTGACCTGCAG 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATTGACTTCAGTAAATGTGCAATACAGAATGCACCAAATCCTGGAGGTGGTGACCTGCAG 420

Qy     454 AAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCCTAAGAAGCTTCCCTGCAGAGGCCAG 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCCTAAGAAGCTTCCCTGCAGAGGCCAG 480

Qy     514 ACTACCTGCCGAGGATCTTGTGATTCTGGAGAACTAGGCCGAAACTCAGGAACATTTTCT 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ACTACCTGCCGAGGATCTTGTGATTCTGGAGAACTAGGCCGAAACTCAGGAACATTTTCT 540

Qy     574 TCGCAGATTGAGAATACACCCATCCTGTGTCCTTTTCATTTGCAACCAGTGCCTGAACCT 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TCGCAGATTGAGAATACACCCATCCTGTGTCCTTTTCATTTGCAACCAGTGCCTGAACCT 600

Qy     634 GAAACAGTGTTAAAAAATCAAGAAGTAGAATTCGGCAGAAATCGAGAGAGGCTTCAGTTT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GAAACAGTGTTAAAAAATCAAGAAGTAGAATTCGGCAGAAATCGAGAGAGGCTTCAGTTT 660

Qy     694 TTTAAGTGGAGTTCAAGAGTTTTAAAGAATGTGGCAGTGATCCCTCCTGGAACTGGAATG 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTAAGTGGAGTTCAAGAGTTTTAAAGAATGTGGCAGTGATCCCTCCTGGAACTGGAATG 720

Qy     754 GCTCATCAAATAAACTTAGAATATTTGTCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTC 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GCTCATCAAATAAACTTAGAATATTTGTCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTC 780

Qy     814 TTCCCAGACAGTGTAGTCGGCACAGATTCACACATAACGATGGTGAATGGTTTAGGGATT 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTCCCAGACAGTGTAGTCGGCACAGATTCACACATAACGATGGTGAATGGTTTAGGGATT 840

Qy     874 CTGGGGTGGGGGGGTTGGAGGCATTGAAACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CTGGGGTGGGGGGTTGGAGGCATTGAAACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCT 900

Qy     934 CTTACTTTACCAGAGGTGGTTGGATGTGAGTTAACTGGGTCATCAAACCCTTTTGTTACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CTTACTTTACCAGAGGTGGTTGGATGTGAGTTAACTGGGTCATCAAACCCTTTTGTTACA 960

Qy     994 TCCATAGATGTTGTTCTTGGTATTACAAAG 1023
           |||||||||||||||||||||||||||||
Db     961 TCCATAGATGTTGTTCTTGGTATTACAAAG 990


RESULT 7
AK027033
LOCUS       AK027033               3341 bp    mRNA    linear   PRI 29-SEP-2000
DEFINITION  Homo sapiens cDNA: FLJ23380 fis, clone HEP16267, highly similar to
            HUMIREBPA Human iron-responsive element-binding protein/iron
            regulatory protein 2 (IRE-BP2/IRP2) mRNA.
ACCESSION   AK027033
VERSION     AK027033.1  GI:10440047
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
            clone:HEP16267.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
            Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
            Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3341)
  AUTHORS   Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
            Shibahara,T., Tanaka,T. and Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure Analysis, Human
            Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
            Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing: Departent of
            Virology and Human Genome Center, Institute of Medical Science,
            University of Tokyo (partly supported by Science and Technology
            Agency).
FEATURES             Location/Qualifiers
     source          1. .3341
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HEP16267"
                     /cell_line="HepG2"
                     /cell_type="hepatoma"
                     /clone_lib="HEP"
                     /note="cloning vector pME18SFL3"
     misc_feature    1. .3341
                     /note="highly similar to HUMIREBPA Human iron-responsive
                     element-binding protein/iron regulatory protein 2
                     (IRE-BP2/IRP2) mRNA"
BASE COUNT     1031 a    597 c    725 g    988 t
ORIGIN

  Query Match             21.7%;  Score 944.2;  DB 9;  Length 3341;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-188;
  Matches  946;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      75 CTTCGATGTATCTAAACTTGGCACCAAGTATGATGTTCTGCCTTACTCAATACGGGTCTT 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTTCGATGTATCTAAACTTGGCACCAAGTATGATGTTCTGCCTTACTCAATACGGGTCTT 60

Qy     135 GTTGGAAGCTGCTGTACGAAATTGTGATGGCTTTTTAATGAAGAAGGAAGATGTTATGAA 194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTTGGAAGCTGCTGTACGAAATTGTGATGGCTTTTTAATGAAGAAGGAAGATGTTATGAA 120
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Qy    195 CATTTTAGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCCTTTTCCCTGCCCGTGT 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CATTTTAGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCCTTTTCCCTGCCCGTGT 180

Qy    255 TCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGCTGCTATGAGGGAGGC 314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTTGCTGCTATGAGGGAGGC 240

Qy    315 AGTGAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTTGTCCGACAGATCTTAC 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTGAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCTTGTCCGACAGATCTTAC 300

Qy    375 AGTTGACCATTCTTTACAAATTGACTTCAGTAAATGTGCAATACAGAATGCACCAAATCC 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGTTGACCATTCTTTACAAATTGACTTCAGTAAATGTGCAATACAGAATGCACCAAATCC 360

Qy    435 TGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCCTAAGAA 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTTAAAGTGCAGCCTAAGAA 420

Qy    495 GCTTCCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTCTGGAGAACTAGGCCG 554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCTTCCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGATTCTGGAGAACTAGGCCG 480

Qy    555 AAACTCAGGAACATTTTCTTCGCAGATTGAGAATACACCCATCCTGTGTCCTTTTCATTT 614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACTCAGGAACATTTTCTTCGCAGATTGAGAATACACCCATCCTGTGTCCTTTTCATTT 540

Qy    615 GCAACCAGTGCCTGAACCTGAAACAGTGTTAAAAAATCAAGAAGTAGAATTCGGCAGAAA 674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAACCAGTGCCTGAACCTGAAACAGTGTTAAAAAATCAAGAAGTAGAATTCGGCAGAAA 600

Qy    675 TCGAGAGAGGCTTCAGTTTTTTAAGTGGAGTTCAAGAGTTTTAAAGAATGTGGCAGTGAT 734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCGAGAGAGGCTTCAGTTTTTTAAGTGGAGTTCAAGAGTTTTAAGAATGTGGCAGTGAT 660

Qy    735 CCCTCCTGGAACTGGAATGGCTCATCAAATAAACTTAGAATATTTGTCAAGAGTGGTTTT 794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCTCCTGGAACTGGAATGGCTCATCAAATAAACTTAGAATATTTGTCAAGAGTGGTTTT 720

Qy    795 TGAAGAAAAAGACCTCCTCTTCCCAGACAGTGTAGTCGGCACAGATTCACACATAACGAT 854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGAAGAAAAAGACCTCCTCTTCCCAGACAGTGTAGTCGGCACAGATTCACACATAACGAT 780

Qy    855 GGTGAATGGTTTAGGGATTCTGGGGTGGGGGGTTGGAGGCATTGAAACAGAAGCAGTTAT 914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGTGAATGGTTTAGGGATTCTGGGGTGGGGGGTTGGAGGCATTGAAACAGAAGCAGTTAT 840

Qy    915 GCTTGGTCTGCCAGTTTCTCTTACTTTACCAGAGGTGGTTGGATGTGAGTTAACTGGGTC 974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCTTGGTCTGCCAGTTTCTCTTACTTTACCGGAGGTGGTTGGATGTGAGTTAACTGGGCC 900

Qy    975 ATCAAACCCTTTTGTTACATCCATAGATGTTGTTCTTGGTATTACAAAG 1023
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Db    901 ATCAAACCCTTTTGTTACATCCATAGATGTTGTTCTTGGTATTACAAAG 949
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RESULT 8
AX377522
LOCUS       AX377522                3770 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 19 from Patent WO0212284.
ACCESSION   AX377522
VERSION     AX377522.1  GI:19573709
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Kirsch,W.M., Lennart,A., Kelln,W.J., Kang,D.K., Levine,R.L. and
            Roualt,T.A.
  TITLE     Iron regulating protein-2 (irp-2) as a diagnostic for
            neurodegenerative disease
  JOURNAL   Patent: WO 0212284-A 19 14-FEB-2002;
            Loma Linda University Medical Center (US) ; THE SECRETARY OF THE
            DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .3770
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
BASE COUNT     1119 a    713 c    840 g   1098 t
ORIGIN
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Query Match 20.2%; Score 877.2; DB 6; Length 3770;
Best Local Similarity 91.6%; Pred. No. 3.2e-174;
Matches 940; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

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Qy      1 ATGGACGCCCCAAAAGCAGGATACGCCTTTGAGTACCTTATTGAAACATTAAATGACAGT 60
          |||||| ||||||  ||||||||| ||||||||||||||||||||||||||||||| ||||
Db     12 ATGGACTCCCCAAGTGCAGGATACACCTTTGAGTACCTTATTGAAACATTAAATGGCAGT 71

Qy     61 TCACATAAGAAGTTCTTCGATGTATCTAAACTT---GGCACCAAGTATGATGTTCTGCCT 117
          ||||| |||||||||||| |||| ||||||||   ||||||||||||||| ||||||||
Db     72 TCACAGAAGAAGTTCTTCAATGTACCTAAACTTGGAGGCACCAAGTATGATATTCTGCCT 131

Qy    118 TACTCAATACGGGTCTTGTTGGAAGCTGCTGTACGAAATTGTGATGGCTTTTTAATGAAG 177
          |||||||||||||| | |||||||||||||||||||||||||||||| ||||||||||
Db    132 TACTCAATACGGGTCCTATTGGAAGCTGCTGTACGAAATTGTGATGGATTTTTAATGAAA 191

Qy    178 AAGGAAGATGTTATGAACATTTTAGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCC 237
          |||||||||||||| || ||||| ||||||||||||||||||||||||||||||||||||
Db    192 AAGGAAGATGTTATAAATATTTTGGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCC 251

Qy    238 TTTTTCCCTGCCCGTGTTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTT 297
          |||||||| |||||||| |||||||||||| |||||||||| ||||||||||||||||||
Db    252 TTTTTCCCCGCCCGTGTTGTTCTTCAAGATTTCACTGGAATACCGGCAATGGTGGATTTT 311

Qy    298 GCTGCTATGAGGGAGGCAGTGAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCT 357
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||||
Db    312 GCTGCTATGAGGGAGGCAATGAAAACTCTTGGAGGTGATCCTAAGAAAGTCCACCCTGCC 371

Qy    358 TGTCCGACAGATCTTACAGTTGACCATTCTTTACAAATTGACTTCAGTAAATGTGCAATA 417
          ||||| |||||||| |||||||||| |||||||| |||||||||||||||||||||||||
Db    372 TGTCCAACAGATCTCACAGTTGACCACTCTTTACAGATTGACTTCAGTAAATGTGCAATA 431

Qy    418 CAGAATGCACCAAATCCTGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTT 477
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    432 CAGAATGCACCAAATCCTGGAGGTGGTGACCTACAGAAAGCAGGAAAGCTCTCTCCACTT 491

Qy    478 AAAGTGCAGCCTAAGAAGCTTCCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGAT 537
          ||||| |||||||||||||||| ||  |||||||||||||||| ||||| ||||||||||
Db    492 AAAGTACAGCCTAAGAAGCTTCCATGTCGAGGCCAGACTACCTGCCGGGGATCGTGTGAT 551

Qy    538 TCTGGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGCAGATTGAGAATACACCCATC 597
          |||||||||||| |||||||||||||||||||||||||||||||||| ||  ||||||||
Db    552 TCTGGAGAACTAAGCCGAAACTCAGGAACATTTTCTTCGCAGATTGAGAATACGCCTGTC 611

Qy    598 CTGTGTCCTTTTCATTTGCAACCAGTGCCTGAACCTGAAACAGTGTTAAAAAATCAAGAA 657
          |||||||| |||||||||||||||||||||||||||||| || ||||||||||||||||||
Db    612 CTGTGTCCCTTTCATTTGCAACCAGTGCCTGAACCTGAGACGGTGTTAAAAAATCAAGAA 671

Qy    658 GTAGAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTAAGTGGAGTTCAAGAGTTTTA 717
          |||||||| |||||||||||||||||||||||| ||||| |||||||| ||| ||| |||
Db    672 GTAGAATTTGGCAGAAATCGAGAGAGGCTTCAATTTTTCAAGTGGAGCTCAGGAGCTTTT 731

Qy    718 AAGAATGTGGCAGTGATCCCTCCTGGAACTGGAATGGCTCATCAAATAAACTTAGAATAT 777
          |||||||||||||| |||||||||||||||||||||||||||||| | |||||||| ||
Db    732 AAGAATGTGGCAGTCATCCCTCCTGGAACTGGAATGGCTCATCAAGTGAACTTAGAACAT 791

Qy    778 TTGTCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTCTTCCCAGACAGTGTAGTCGGCACA 837
          ||||| ||||| || |||||||||   ||||| ||||||||||||| ||| | ||||||
Db    792 TTGTCGAGAGTAGTGTTTGAAGAAGCCGACCTGCTCTTCCCAGACAGCGTAATTGGCACA 851

Qy    838 GATTCACACATAACGATGGTGAATGGTTTAGGGATTCTGGGGTGGGGGGTTGGAGGCATT 897
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Db    852 GATTCTCATATAACCATGGTGAATGGATTGGGAATTCTTGGGTGGGGAGTTGGAGGCATT 911

Qy    898 GAAACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTCTTACTTTACCAGAGGTGGTTGGA 957
          || ||||| |||||||||||||| |||||||| ||||||||||||||||||||||||||||
Db    912 GAGACAGAGGCAGTTATGCTTGGCCTGCCAGTTACTCTTACTTTACCAGAGGTGGTTGGA 971

Qy    958 TGTGAGTTAACTGGGTCATCAAACCCTTTTGTTACATCCATAGATGTTGTTCTTGGTATT 1017
          |||||| |||||||||||||| ||  |||||||||||||||||||| |||| || || |||
Db    972 TGTGAGCTAACTGGGTCATCCAATGCTTTTGTTACATCCATAGATATTGTCCTAGGCATT 1031

Qy   1018 ACAAAG 1023
          ||||||
Db   1032 ACAAAG 1037


RESULT 9
RNU20181
LOCUS       RNU20181               3770 bp    mRNA    linear   ROD 26-OCT-1995
DEFINITION  Rattus norvegicus iron-regulatory protein 2 (IRP2) mRNA, complete
            cds.
ACCESSION   U20181
VERSION     U20181.1  GI:897582
KEYWORDS    .
SOURCE      rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3770)
  AUTHORS   Guo,B., Brown,F.M., Phillips,J.D., Yu,Y. and Leibold,E.A.
  TITLE     Characterization and expression of iron regulatory protein 2
            (IRP2). Presence of multiple IRP2 transcripts regulated by
            intracellular iron levels
  JOURNAL   J. Biol. Chem. 270 (28), 16529-16535 (1995)
  MEDLINE   95348066
   PUBMED   7622457
REFERENCE   2  (bases 1 to 3770)
  AUTHORS   Brown,F.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1995) Fritz M. Brown, Program in Hum. Mol. Biol.
            and Genetics, University of Utah, 3250 Bldg 533, Salt Lake City, UT
            84112, USA
FEATURES             Location/Qualifiers
     source          1. .3770
                     /organism="Rattus norvegicus"
                     /strain="Spraque-Dawley"
                     /db_xref="taxon:10116"
                     /clone="pSL800, pUZB2-1"
                     /sex="male"
                     /tissue_type="liver"
                     /dev_stage="adult"
                     /note="Similar to GenBank Accession No. U20180"
     gene            1. .3770
                     /gene="IRP2"
     CDS             12. .2903
                     /gene="IRP2"
                     /codon_start=1
                     /product="iron-regulatory protein 2"
                     /protein_id="AAA79927.1"
                     /db_xref="GI:897583"
                     /translation="MDSPSAGYTFEYLIETLNGSSQKKFFNVPKLGGTKYDILPYSIR
                     VLLEAAVRNCDGFLMKKEDVINILDWKTKQSNVEVPFFPARVVLQDFTGIPAMVDFAA
                     MREAMKTLGGDPKKVHPACPTDLTVDHSLQIDFSKCAIQNAPNPGGGDLQKAGKLSPL
                     KVQPKKLPCRGQTTCRGSCDSGELSRNSGTFSSQIENTPVLCPFHLQPVPEPETVLKN
                     QEVEFGRNRERLQFFKWSSGAFKNVAVIPPGTGMAHQVNLEHLSRVVFEEADLLFPDS
                     VIGTDSHITMVNGLGILGWGVGGIETEAVMLGLPVTLTLPEVVGCELTGSSNAFVTSI
                     DIVLGITKHLRQVGVAGKFVEFFGSGVSQLSIVDRTTIANMCPEYGAILSFFPVDNVT
                     LRHLEHTGFDKTKLESMEEYLKAVKLFRNDENSSEPEYSQVIQINLNSIVASVSGPKR
                     PQDRVAVTDMKSDFQACLNEKVGFKGFQVAAEKQSDTVSVRYDGSEYKLSHGSVVIAA
                     VISCTNNCNPSVMLAAGLLAKKAVETGLRVKPYIRTSLSPGSGMVTHYLSSSGVLPYL
                     SKLGFEIVGYGCSTCVGNTAPLSEAILNAVKQGDLATCGVLSGNKNFEGRLCDCVRAN
                     YLASPPLVVAYAIAGTVNIDFQTEPLGTDSTGKNIYLHDIWPSREEVHQIEEEHVILS
                     MFKALKEKVEMGNKRWNSLDAPDSVLFPWDVKSTYIRCPSFFDKLTKEPAASQPIENA
                                    HVLLYLGDSVTTDHISPAGSIARSRAAAKYLTNRGLTPREFNSYGARRGNDAVMTRGT
                                    FANIKLFNKFIGKPAPKTIHFPSGQTLDVFEAAELYQKEGIPLIILAGKKYGSGNSRD
                                    WAAKGPYLLGVKAVLAESYEKIHKDHLIGIGIAPLEFLPGENADSLGLSGREVFSLSF
                                    PEELFPGITLNIKTSTGKEFSVIAAFENDVEITLYKHGGLLNFVARKFL"
BASE COUNT      1119 a    713 c    840 g    1098 t
ORIGIN

  Query Match             20.2%;  Score 877.2;  DB 10;  Length 3770;
  Best Local Similarity   91.6%;  Pred. No. 3.2e-174;
  Matches  940;  Conservative    0;  Mismatches   83;  Indels    3;  Gaps    1;

Qy      1 ATGGACGCCCCAAAAGCAGGATACGCCTTTGAGTACCTTATTGAAACATTAAATGACAGT 60
          |||||| ||||||  ||||||||| ||||||||||||||||||||||||||||||| ||||
Db     12 ATGGACTCCCCAAGTGCAGGATACACCTTTGAGTACCTTATTGAAACATTAAATGGCAGT 71

Qy     61 TCACATAAGAAGTTCTTCGATGTATCTAAACTT---GGCACCAAGTATGATGTTCTGCCT 117
          ||||| |||||||||||| |||||  ||||||||   ||||||||||||||| ||||||||
Db     72 TCACAGAAGAAGTTCTTCAATGTACCTAAACTTGGAGGCACCAAGTATGATATTCTGCCT 131

Qy    118 TACTCAATACGGGTCTTGTTGGAAGCTGCTGTACGAAATTGTGATGGCTTTTTAATGAAG 177
          ||||||||||||||| | |||||||||||||||||||||||||||||| ||||||||||
Db    132 TACTCAATACGGGTCCTATTGGAAGCTGCTGTACGAAATTGTGATGGATTTTTAATGAAA 191

Qy    178 AAGGAAGATGTTATGAACATTTTAGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCC 237
          |||||||||||||| || ||||| |||||||||||||||||||||||||||||||||||
Db    192 AAGGAAGATGTTATAAATATTTTGGACTGGAAAACCAAACAAAGCAATGTTGAAGTGCCC 251

Qy    238 TTTTTCCCTGCCCGTGTTCTTCTTCAAGATTTTACTGGAATACCAGCAATGGTGGATTTT 297
          |||||||| ||||||||| |||||||||||| |||||||||||||| ||||||||||||
Db    252 TTTTTCCCCGCCCGTGTTGTTCTTCAAGATTTCACTGGAATACCGGCAATGGTGGATTTT 311

Qy    298 GCTGCTATGAGGGAGGCAGTGAAAACTCTTGGAGGTGATCCTGAGAAAGTCCATCCTGCT 357
          |||||||||||||||| |||||||||||||||||||||| |||||||||| |||||
Db    312 GCTGCTATGAGGGAGGCAATGAAAACTCTTGGAGGTGATCCTAAGAAAGTCCACCCTGCC 371

Qy    358 TGTCCGACAGATCTTACAGTTGACCATTCTTTACAAATTGACTTCAGTAAATGTGCAATA 417
          ||||| |||||||| |||||||||| |||||||| ||||||||||||||||||||||||
Db    372 TGTCCAACAGATCTCACAGTTGACCACTCTTTACAGATTGACTTCAGTAAATGTGCAATA 431

Qy    418 CAGAATGCACCAAATCCTGGAGGTGGTGACCTGCAGAAAGCAGGAAAGCTCTCTCCACTT 477
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    432 CAGAATGCACCAAATCCTGGAGGTGGTGACCTACAGAAAGCAGGAAAGCTCTCTCCACTT 491

Qy    478 AAAGTGCAGCCTAAGAAGCTTCCCTGCAGAGGCCAGACTACCTGCCGAGGATCTTGTGAT 537
          ||||| |||||||||||||||| ||  |||||||||||||||||| ||||| ||||||
Db    492 AAAGTACAGCCTAAGAAGCTTCCATGTCGAGGCCAGACTACCTGCCGGGGATCGTGTGAT 551

Qy    538 TCTGGAGAACTAGGCCGAAACTCAGGAACATTTTCTTCGCAGATTGAGAATACACCCATC 597
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||| ||  ||
Db    552 TCTGGAGAACTAAGCCGAAACTCAGGAACATTTTCTTCGCAGATTGAGAATACGCCTGTC 611

Qy    598 CTGTGTCCTTTTCATTTGCAACCAGTGCCTGAACCTGAAACAGTGTTAAAAAATCAAGAA 657
          |||||||| |||||||||||||||||||||||||| || ||||||||||||||||||||
Db    612 CTGTGTCCCTTTCATTTGCAACCAGTGCCTGAACCTGAGACGGTGTTAAAAAATCAAGAA 671

Qy    658 GTAGAATTCGGCAGAAATCGAGAGAGGCTTCAGTTTTTTAAGTGGAGTTCAAGAGTTTTA 717
          |||||||| ||||||||||||||||||||| ||||| |||||||| ||| ||| |||||
Db    672 GTAGAATTTGGCAGAAATCGAGAGAGGCTTCAATTTTTCAAGTGGAGCTCAGGAGCTTTT 731

Qy    718 AAGAATGTGGCAGTGATCCCTCCTGGAACTGGAATGGCTCATCAAATAAACTTAGAATAT 777
          |||||||||||||| |||||||||||||||||||||||||||||| | ||||||||| ||
Db    732 AAGAATGTGGCAGTCATCCCTCCTGGAACTGGAATGGCTCATCAAGTGAACTTAGAACAT 791

Qy    778 TTGTCAAGAGTGGTTTTTGAAGAAAAAGACCTCCTCTTCCCAGACAGTGTAGTCGGCACA 837
          ||||| ||||| || |||||||||   ||||| ||||||||||||||| ||| | ||||||
Db    792 TTGTCGAGAGTAGTGTTTGAAGAAGCCGACCTGCTCTTCCCAGACAGCGTAATTGGCACA 851

Qy    838 GATTCACACATAACGATGGTGAATGGTTTAGGGATTCTGGGGTGGGGGGTTGGAGGCATT 897
          ||||| || ||||| |||||||||||| || || ||||| |||||||| ||||||||||||
Db    852 GATTCTCATATAACCATGGTGAATGGATTGGGAATTCTTGGGTGGGGAGTTGGAGGCATT 911

Qy    898 GAAACAGAAGCAGTTATGCTTGGTCTGCCAGTTTCTCTTACTTTACCAGAGGTGGTTGGA 957
          || ||||| |||||||||||||| |||||||| ||||||||||||||||||||||||||||
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Db    912 GAGACAGAGGCAGTTATGCTTGGCCTGCCAGTTACTCTTACTTTACCAGAGGTGGTTGGA 971

Qy    958 TGTGAGTTAACTGGGTCATCAAACCCTTTTGTTACATCCATAGATGTTGTTCTTGGTATT 1017
          |||||| |||||||||||||| ||  ||||||||||||||||||| |||| || || |||
Db    972 TGTGAGCTAACTGGGTCATCCAATGCTTTTGTTACATCCATAGATATTGTCCTAGGCATT 1031

Qy   1018 ACAAAG 1023
          ||||||
Db   1032 ACAAAG 1037


RESULT 10
AC004469/c
LOCUS       AC004469               309662 bp    DNA     linear   HTG 15-NOV-2000
DEFINITION  Homo sapiens clone CTB-58E15, WORKING DRAFT SEQUENCE, 126 unordered
            pieces.
ACCESSION   AC004469
VERSION     AC004469.8  GI:11141978
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 309662)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
            Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
            Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
            Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
            Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
            Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
            Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
            Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
            Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
            Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
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            Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
            Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
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            Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
            Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
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            Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
            Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
            Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
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            Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
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            Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
            Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
            and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 309662)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-1998) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 14, 2000 this sequence version replaced gi:11079386.
            ---------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            ---------- Project Information
                Center project name: WO
                Center clone name: CTB-58E15
            ---------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-primer Bodipy: 10% of reads
                Chemistry: Dye-terminator Big Dye: 24% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 263288 bases at least Q40
                Consensus quality: 281803 bases at least Q30
                Consensus quality: 292338 bases at least Q20
                Estimated insert size: 261499; sum-of-contigs estimation
                Quality coverage: 12.9x in Q20 bases; sum-of-contigs estimation
            ----------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * NOTE: This sequence may represent more than one clone.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 126 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1      7683: contig of 7683 bp in length
            *     7684      7783: gap of unknown length
            *     7784     12646: contig of 4863 bp in length
            *    12647     12746: gap of unknown length
            *    12747     19521: contig of 6775 bp in length
            *    19522     19621: gap of unknown length
            *    19622     26379: contig of 6758 bp in length
            *    26380     26479: gap of unknown length
            *    26480     32210: contig of 5731 bp in length
            *    32211     32310: gap of unknown length
            *    32311     38553: contig of 6243 bp in length
            *    38554     38653: gap of unknown length
            *    38654     42723: contig of 4070 bp in length
            *    42724     42823: gap of unknown length
            *    42824     45575: contig of 2752 bp in length
            *    45576     45675: gap of unknown length
            *    45676     50160: contig of 4485 bp in length
            *    50161     50260: gap of unknown length
            *    50261     54295: contig of 4035 bp in length
            *    54296     54395: gap of unknown length
            *    54396     59661: contig of 5266 bp in length
            *    59662     59761: gap of unknown length
            *    59762     63562: contig of 3801 bp in length
            *    63563     63662: gap of unknown length
            *    63663     67444: contig of 3782 bp in length
            *    67445     67544: gap of unknown length
            *    67545     72937: contig of 5393 bp in length
            *    72938     73037: gap of unknown length
            *    73038     77291: contig of 4254 bp in length
            *    77292     77391: gap of unknown length
            *    77392     81075: contig of 3684 bp in length
            *    81076     81175: gap of unknown length
            *    81176     84196: contig of 3021 bp in length
            *    84197     84296: gap of unknown length
            *    84297     88351: contig of 4055 bp in length
            *    88352     88451: gap of unknown length
            *    88452     91923: contig of 3472 bp in length
            *    91924     92023: gap of unknown length
            *    92024     96830: contig of 4807 bp in length
            *    96831     96930: gap of unknown length
            *    96931    101888: contig of 4958 bp in length
            *   101889    101988: gap of unknown length
            *   101989    105510: contig of 3522 bp in length
            *   105511    105610: gap of unknown length
            *   105611    108586: contig of 2976 bp in length
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